

BLASTN 2.2.1 [Apr-13-2001]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Sch?ffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997). "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1009527356-10099-15388

Query=

(1440 letters)

Database: All GenBank+EMBL+DBJ+PDB sequences (but no EST, STS, GSS, or phase 0, 1 or 2 HTGS sequences).

1,073,652 sequences; 4,829,212,789 total letters

If you have any problems or questions with the results of this search please refer to the BLAST FAQs

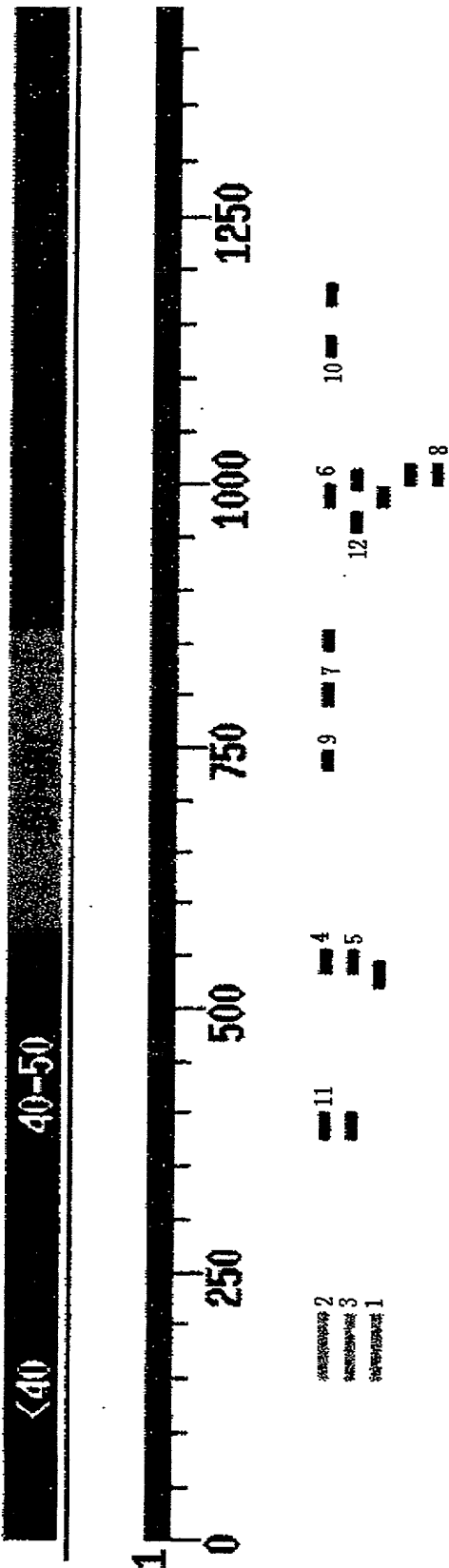
Taxonomy reports

Distribution of 19 Blast Hits on the Query Sequence

Sequences producing significant alignments:			Score (bits)	E Value
1	gi 9628890 ref NC_001723.1	Peanut stripe virus, complete g...	68	2e-08
2	gi 1016234 gb U34972.1 PSU34972	Peanut stripe virus mRNA po...	68	2e-08
3	gi 1335723 gb U05771.1 PSU05771	Peanut stripe virus, comple...	68	2e-08
4	gi 15642775 ref NC_000853.1	Thermotoga maritima, complete ...	44	0.36
5	gi 4980775 gb AE001710.1 AE001710	Thermotoga maritima secti...	44	0.36
6	gi 16973823 emb AL354976.1 AL354976	Human DNA sequence fro...	42	1.4
7	gi 7838255 emb AL132822.15 HSJ1017F8	Human DNA sequence fro...	42	1.4
8	gi 15341592 gb AC018499.3	Homo sapiens chromosome 3 clone ...	40	5.6
9	gi 14589685 gb AC008167.5	Homo sapiens BAC clone RP11-1720...	40	5.6
10	gi 16445165 gb AC092038.3	Homo sapiens chromosome 3 clone ...	40	5.6
11	gi 15020311 gb AY040316.1	Hylurdretonus araucariae elonga...	40	5.6
12	gi 14670056 gb AC073614.17 AC073614	Homo sapiens Xp BAC RP1...	40	5.6

Fig.1a

Color Key for Alignment Scores



Sequence	Alignment Score
1-3	50-80
4-12	40-50

Fig.1b

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RID: 1010120805-18751-22816

Query=

(882 letters)

Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, or phase 0, 1 or 2 HTGS sequences).
1,079,316 sequences; 4,832,507,720 total letters

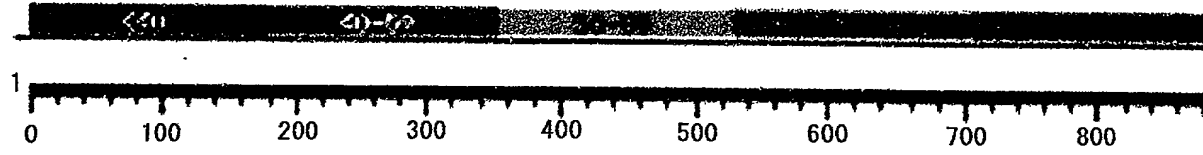
If you have any problems or questions with the results of this search please refer to the BLAST FAQs

Taxonomy reports

Distribution of 143 Blast Hits on the Query Sequence

Fig.2a

Color Key for Alignment Score



↑
PLDMV

Alignment Score 50-80
Alignment Score 80-200



Fig.2b

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RID: 1010127418-14473-18661

Query=

(1374 letters)

Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, or phase 0, 1 or 2 HTGS sequences).

1,079,316 sequences; 4,832,507,720 total letters

If you have any problems or questions with the results of this search please refer to the BLAST FAQs

Taxonomy reports

Distribution of 99 Blast Hits on the Query Sequence

Fig.3a

Color Key for Alignment Scores

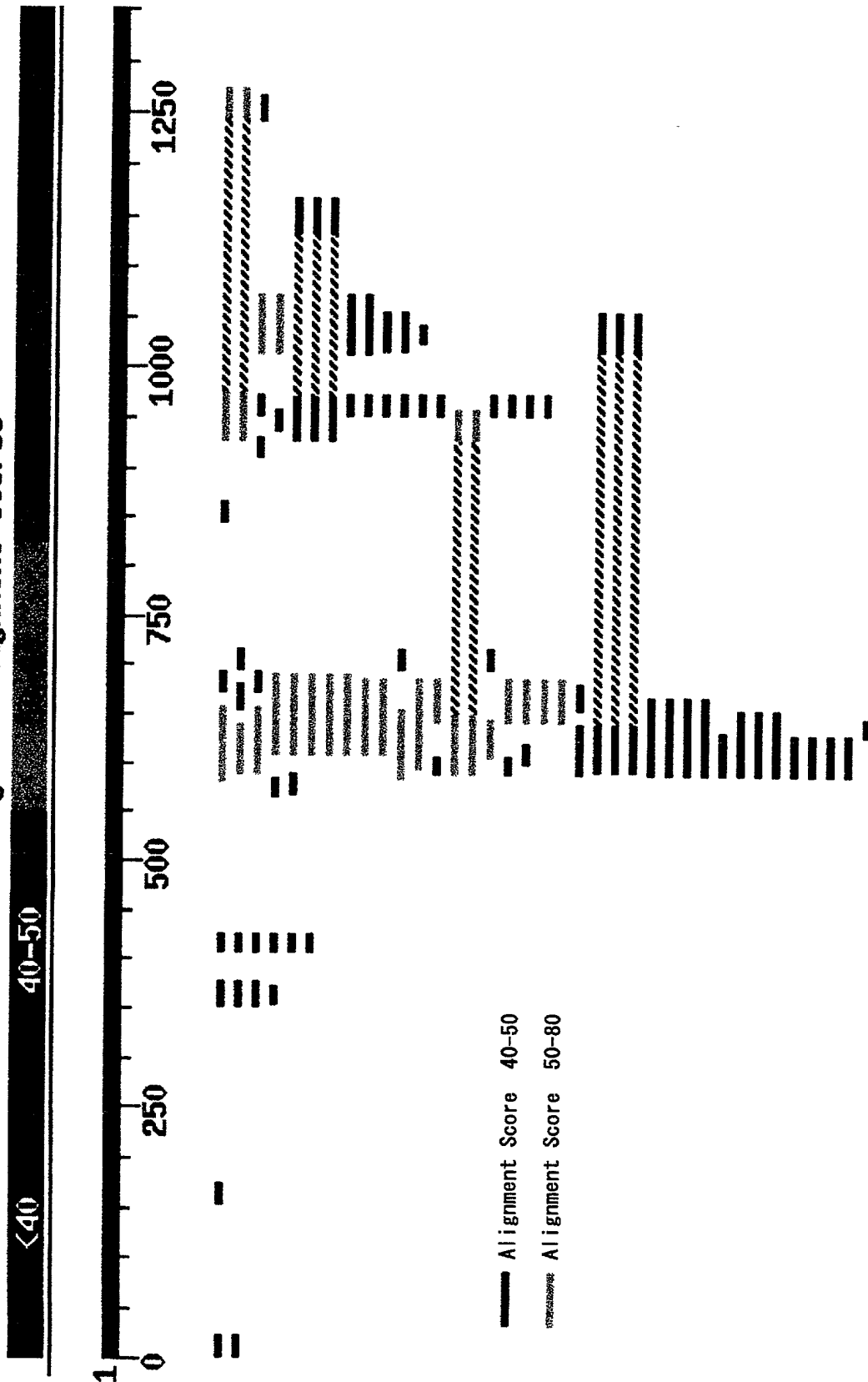


Fig.3b

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Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs", Nucleic Acids Res. 25:3389-3402.

RID: 1010128690-26317-13567

Query=

(1563 letters)

Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS,
GSS, or phase 0, 1 or 2 HTGS sequences).
1,079,316 sequences; 4,832,507,720 total letters

If you have any problems or questions with the results of this search
please refer to the BLAST FAQs

Taxonomy reports

Distribution of 175 Blast Hits on the Query Sequence

Fig.4a

20050620 065900T

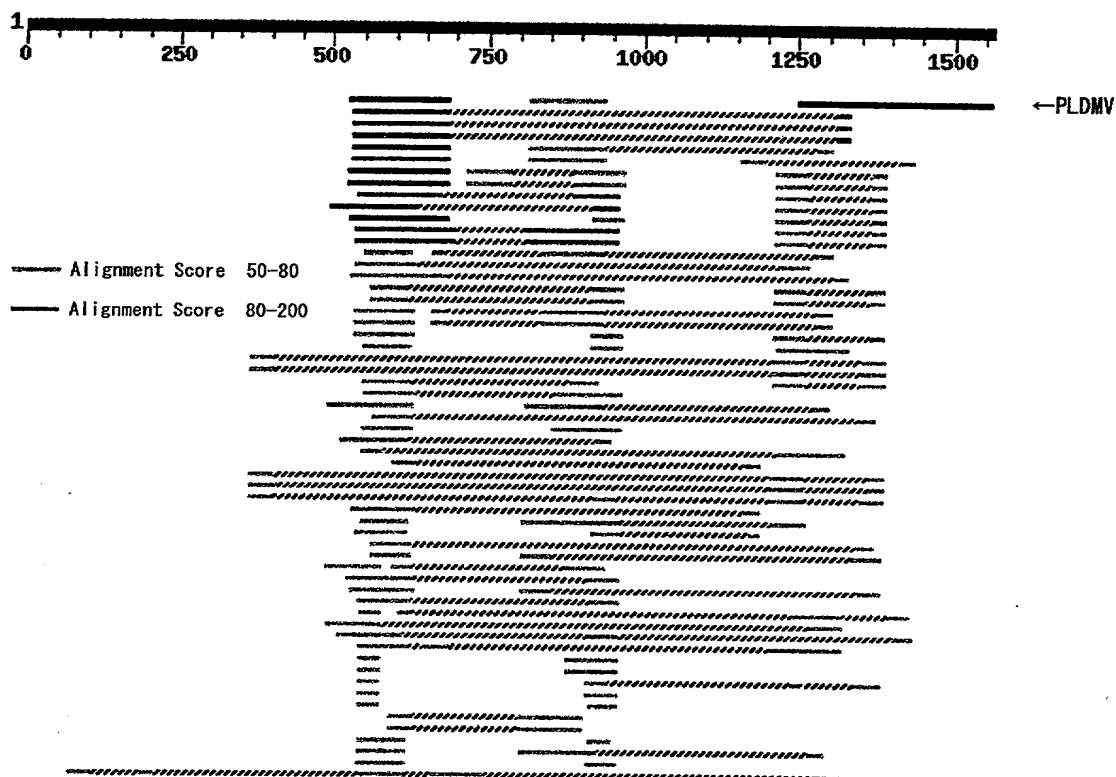


Fig.4b